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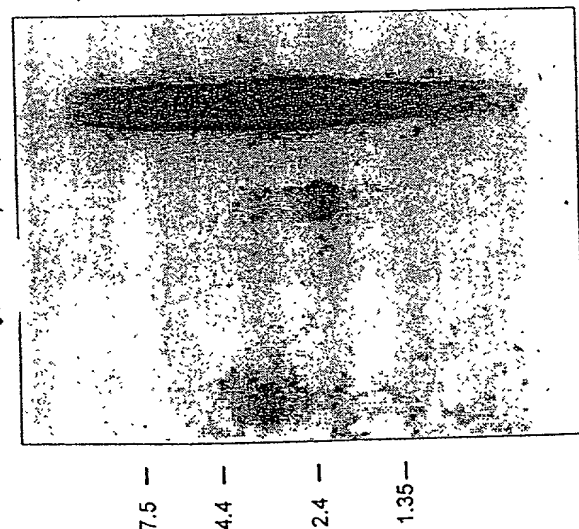
TM5

TM6

presumed pore region

OTRPC4  
MAGETAVGQWMSKLEAKKHSNKKKQWATTAEDIPERPVFLPKKAEKRSGLIVTKSSDGGTFFDR

heart  
brain  
spleen  
lung  
liver  
skeletal muscle  
kidney  
testicle



CTCGGCGGAGGATCAGGAAGGCGCGCTGCGCCCCCGCTCTGAGGCTGAGAAGTACAACAGATCTGGGTCAGATATGGCAGATCTGGTGA TGGTCCCGGTGCACGCGCTGGGGAGGTGGCTGAGCCCTGGAG 140  
GAGCCGGGCTCCCTAGTCCCTTCGCGGCGCGGACGCGGGGCGCAGGACTCCGACTTCTCATGTTTGCTAGACCCAGGTCTACCGTCTAGGACCACTACCGGGGCACGTGCGGACCCCTCCACCGACTCGGGGACCTC

5-RACE-Fragment

M A D P G D G P R A A P G E V A E P P G

OTR-PC-ORF

Aat II  
 Nhe I  
 ATGAGAGTGGTACCTCTGGTGGGAGGCCCTCCCCCTCTCTCCCTGGCCAACTCTTTGAGGGGAGAGGCTCCTCTCTCTTCCCGGTGGATGCTAGCCGCCCTGCTGGCCCTGGCGATGGAGCTCCAAAGCTG  
 TACTCTCACCATTGAGACCAACCCCTCCGGAAGGGGAGAGAGGGACCGGTTAGACAACCTCCCTCTCCGAGGAGAGAGAAGGGGCCACTTACGATCGCGGAGCGAGCCGGGACCCTACTCTGCAGGTTTGGAC  
 280

DESSGTS GGEEA F P L S S L A N L F E E G F F G S S S L S P V D A S R P A G P G D G R P N L

Bsp120 I  
 Apa I  
 420  
 CGTATGAAGTTCAGGGCGCTTCCGCAAGGGGTTCCCAACCCCATTGACCTGTTGGAGTCCACCCGGTACGAGTCCTCAGTAGTGCTGGCCCAAGAAAGCCGCCATGGATTCTTGTTCGACTACGGCACTTACCG  
 GCATATTCAAGTCCCAGCAAGGCTTCCCCCAAGGTTGGGGTAAC TGGACAACCTCAGGTGGGCCATGCTCAGGAGTCATCAGGACCCGGGTCTTTGCGGGGTACCTAAGGAACAAGCTGATGCCCGTGAATGGC  
 5-PACE Fragment  
 R M K F Q G A F R K G V P N P I D L L E S T R Y F S S V V P G P K K A P M D S L F D Y G T Y R  
 EST

EclHK I  
 Xma I  
 Sma I  
 TCACCACCCAGTGACAACAAGAGATGGAGGAGAAAGBTCTGGAGAGAGCAGCCACAGAGCCCCAAAGTCTCTGCCCCAGCCCATCCCTCAAAAGTCTTCAATCGGGCCCATCTCTTTGACATTTGTGTCGGGG 560

H H P S D N K R W R R K V V E K Q P Q S P K A P A P Q P P I L K V F N R P I L F D I V S R

INTRON  
INTRON 5956bpHS

Fig. 2a (I)

INTROJ 84 ALBAJE

## Test

840  
GACACCA TCCGGTGTTC TGGACATT GCGAGCGCAGCGGCAACA TCGTGTAATT CATCAACT GCGCCCTTCAGAGACATCTACTACGAGGCCAGACATCCCTGCACATTCGCATCGAACGGCGCTGCAAGCACATACGT  
CTGTGGTAGGGCCACAACGACCTGTAAAGCCCTCGCGTGGCCGTTG TACGCACTTAAGTAGTTGAGCGGGGAAGTCTCTGTAGATGA TGGCTCCGGTCTGTAGGAGACGTGTAAACGGTAGGCTTGCCCGGACGTTCTGTGATGCA


SYNOPSIS

## TEST

**INTRON** 

**Ankyrin domain**

GGAGGCTGCTGGTGGCCCCAGGGAGCGGAGCTGACGCGCCAGGCCCGCTCTTCCAGCCCAAGGATGAGGAGGCTACTTCTACTTTGGGAGCTGCCCTGTCCCTGGCAGCCTGCACCAACGACCGCACATCG  
980



NTBON 1704bp/HS

EE LL V A O G A D V H A Q A R G R F F O P K D F G G Y F Y F G E L P L S L A A C T N Q P H I I  
OTRC4-DRF

153

**Ankyrin** ■  
Ankyrin domain

Xho I

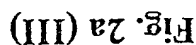
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AGT TGA TGA G A C T C T C T T G S A G T G T C T T T G S A C T G T A C T C C G C T G T C C C C C T T G T G C C A C A C A G T G C G C G A C C A C C G T A G C G C T G T T G T G G G C T C T T G T G G T T C A A C A A G T G G T T C T A C A T G C T G  
1120

157

VVNNYYLTTEENPHKKKADMMRRRODSRGN<sup>1</sup>YV<sup>1</sup>HALVAIAADNTRRENTKFFVTCKMYD

— Ankyrin domain —

Fig. 2a (II)



K K C P G V N S L F V D G S F O L L Y F I Y S V L V V V S A A L Y L A G I E A Y L A V M V F  
 EST  
 OTFC-ORF  
 transmembrane  
 transmembrane region  
 transmembrane  
 transmembrane region  
 transmembrane  
 transmembrane region

CCCTGGTCTCGGCTGGATGGCGTGACTTCAGCGCGGGTTBAAGCTGACGGGACCACAGCATCATGATTCAAGAAGATCCTCTTCAAAGACCTCTTCCGCTTGTGTACTGCTCTTTCATGATCGGC  
GGGACCGAGCACCGACCTACTTACGGACATGAAGTCGCGGCCCAACTTCGACTGCCCCCTGGATGTCGTAGTACTAAGTCTTCTGAGAGAAGTTTCTGGAAGGCGAAGCGAACACACATGGACGAGAAGTACTAGCGG

A L V L G W M N A L Y F T R G L K L T G T Y S I Q K I L F K D L F R F L L V Y L L F H I G

EST ORP4orf6

transmembrane transmembrane region

(iron 281bp+8)

107

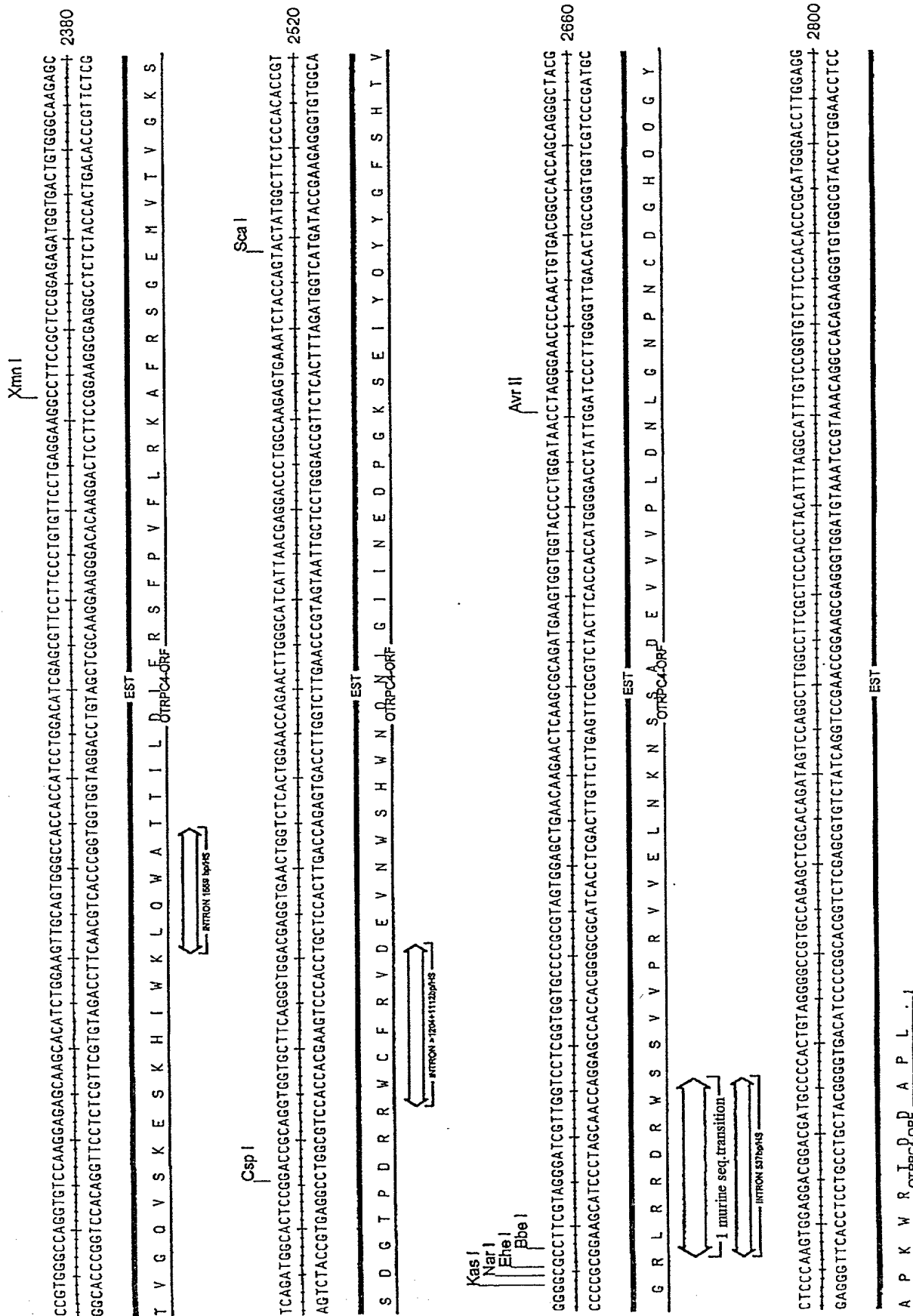
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 2100  
 ATACCGAGTCGGGACCAAGTGGAGGACTTAGGCACGGTGTGACTTCCAGACACTGCTCCTGGTCTGCTTGACGTGCCACGGGTGCATAGGACGACACGGCGCTGTCGCTCTGGAAGTCGCGGAAGGAGGACCTTGGAGAA  
 \_\_\_\_\_ EST \_\_\_\_\_  
 Y A S A L V T L L N P C T N M K V C D E D Q S N <sup>1</sup> <sub>108</sub> <sup>109</sup> <sub>110</sub> <sup>111</sup> <sub>112</sub> <sup>113</sup> <sub>114</sub> <sup>115</sup> <sub>116</sub> <sup>117</sup> <sub>118</sub> <sup>119</sup> <sub>120</sub> <sup>121</sup> <sub>122</sub> <sup>123</sup> <sub>124</sub> <sup>125</sup> <sub>126</sub> <sup>127</sup> <sub>128</sub> <sup>129</sup> <sub>130</sub> <sup>131</sup> <sub>132</sub> <sup>133</sup> <sub>134</sub> <sup>135</sup> <sub>136</sub> <sup>137</sup> <sub>138</sub> <sup>139</sup> <sub>140</sub> <sup>141</sup> <sub>142</sub> <sup>143</sup> <sub>144</sub> <sup>145</sup> <sub>146</sub> <sup>147</sup> <sub>148</sub> <sup>149</sup> <sub>150</sub> <sup>151</sup> <sub>152</sub> <sup>153</sup> <sub>154</sub> <sup>155</sup> <sub>156</sub> <sup>157</sup> <sub>158</sub> <sup>159</sup> <sub>160</sub> <sup>161</sup> <sub>162</sub> <sup>163</sup> <sub>164</sub> <sup>165</sup> <sub>166</sub> <sup>167</sup> <sub>168</sub> <sup>169</sup> <sub>170</sub> <sup>171</sup> <sub>172</sub> <sup>173</sup> <sub>174</sub> <sup>175</sup> <sub>176</sub> <sup>177</sup> <sub>178</sub> <sup>179</sup> <sub>180</sub> <sup>181</sup> <sub>182</sub> <sup>183</sup> <sub>184</sub> <sup>185</sup> <sub>186</sub> <sup>187</sup> <sub>188</sub> <sup>189</sup> <sub>190</sub> <sup>191</sup> <sub>192</sub> <sup>193</sup> <sub>194</sub> <sup>195</sup> <sub>196</sub> <sup>197</sup> <sub>198</sub> <sup>199</sup> <sub>200</sub> <sup>201</sup> <sub>202</sub> <sup>203</sup> <sub>204</sub> <sup>205</sup> <sub>206</sub> <sup>207</sup> <sub>208</sub> <sup>209</sup> <sub>210</sub> <sup>211</sup> <sub>212</sub> <sup>213</sup> <sub>214</sub> <sup>215</sup> <sub>216</sub> <sup>217</sup> <sub>218</sub> <sup>219</sup> <sub>220</sub> <sup>221</sup> <sub>222</sub> <sup>223</sup> <sub>224</sub> <sup>225</sup> <sub>226</sub> <sup>227</sup> <sub>228</sub> <sup>229</sup> <sub>230</sub> <sup>231</sup> <sub>232</sub> <sup>233</sup> <sub>234</sub> <sup>235</sup> 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CAAGCTCACCATCGGCATGGGAGACCTGGAGATGCTGAGCAGCGCAAGTACCCGGGTCTTCATCTCCTGCTGGTCACTACATCATCTCTGCTCGTGTGAACATGCTTATCGCCCTCATGGGTGAGA  
 GTTCGAGTGGTAGCCGTACCCCTCTGACACTCTACGACTCGTGCGGTTCATGGGGCAACCAGAAGTAGGAGGACGACCAGTGGATGTAGTAGGAGTGGAAAGCAGGAGCAACTTGTACGAATAGCGGAGTACCCCACTCT

K L T I G M G D L E M L S S A K Y P V V F OTRPC4orf EST V T Y I I L T F V L L L N M L I A L M G E

transmembrane  
 transmembrane region

Fig. 2a (IV)



TGAGGGCCCTGTGGCGACTCTGTGGAGGCCGACAGGACCTCTGGTCCCGCCGCAAGACTTTTGCTTCAGCTCTACTCCCCACATGGGGGGGGGGGCTCTCTGGCTACCTGTCTTCGCTCGCTCCCATGGAGTCACCTAAG  
 ACTCCCGGAGACACCCGCTGAGACACTCGGGGGTCTCTGGGAGACACAGGGGGCGGTCTTGAAACCGGAAGTCGAGATGAGGGGTGTAACCCCCCGCCGAGGACCCGATGGACACAGAGCGAGGGGTACCTTCAGTGGATTC

EST

CCAGCACAGGCCCTCTCCTCGAAGGTCAGGCCCATCCCTCTGTGTATTATTATTCCTCCTCAGGAAATGGGGTGGCAGGAGTCACCCCGCGCTGGAACTGGCCAGGCTGAAGCTCATGCAGGACGC  
GGGTGCTGTTCCGGGAGAGAGCTTTCGAGTCCGGGGTAGGGAGAACACAATAATAACGAGAGGAGTCTTTTACCCCACTCCCTCAGGTGGGGCCGACCTTGGACCCGCTCCGAGTACGTCCCTGCGG

**EST**

3220  
TGCAGCTCCGACCTGCCACAGATCTGACCTGCTGCAGCCCTGGCTAGTGGGTCTCTGACTTGAAGAGATCGGGGCGCTGGTCTCAATAATGTTATTCTCGGTGAAAAAATAAAAAA  
AGCTCAGGCTGACGGTCTAGACTGACAGCGTGGGGACCGATCACACCAGAACAGACATGAACCTCTCTAGCCCGGCGACACAGAGTATTACAAATAAGAGCCACCTTTTTTTTTTTTTTTT

153

EST.

Fig. 2a (VI)

Fig. 2b

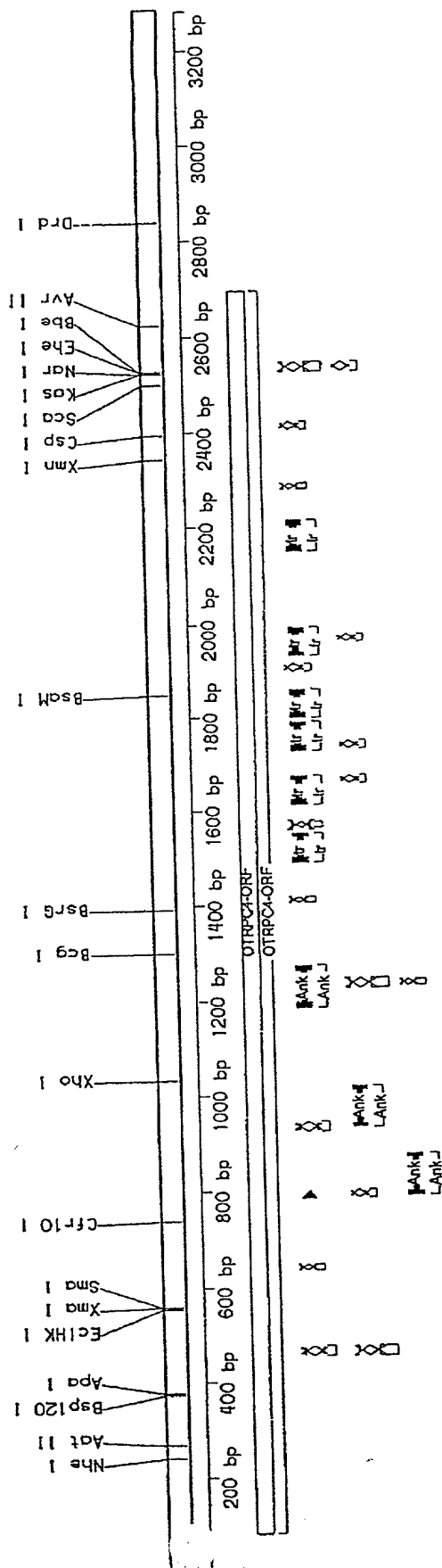




Fig. 3a

Mouse kidney, sagittal section



106100 641360

Mouse kidney, sagittal section

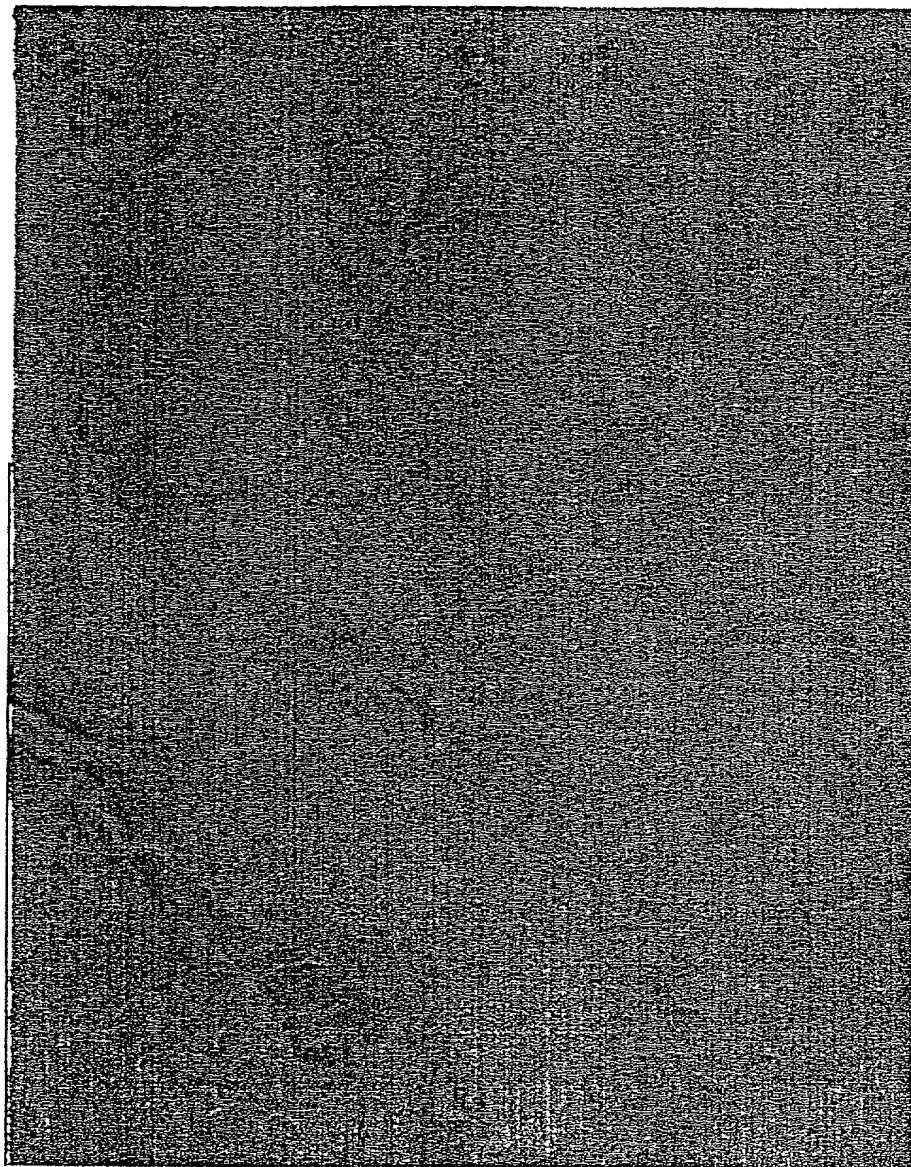
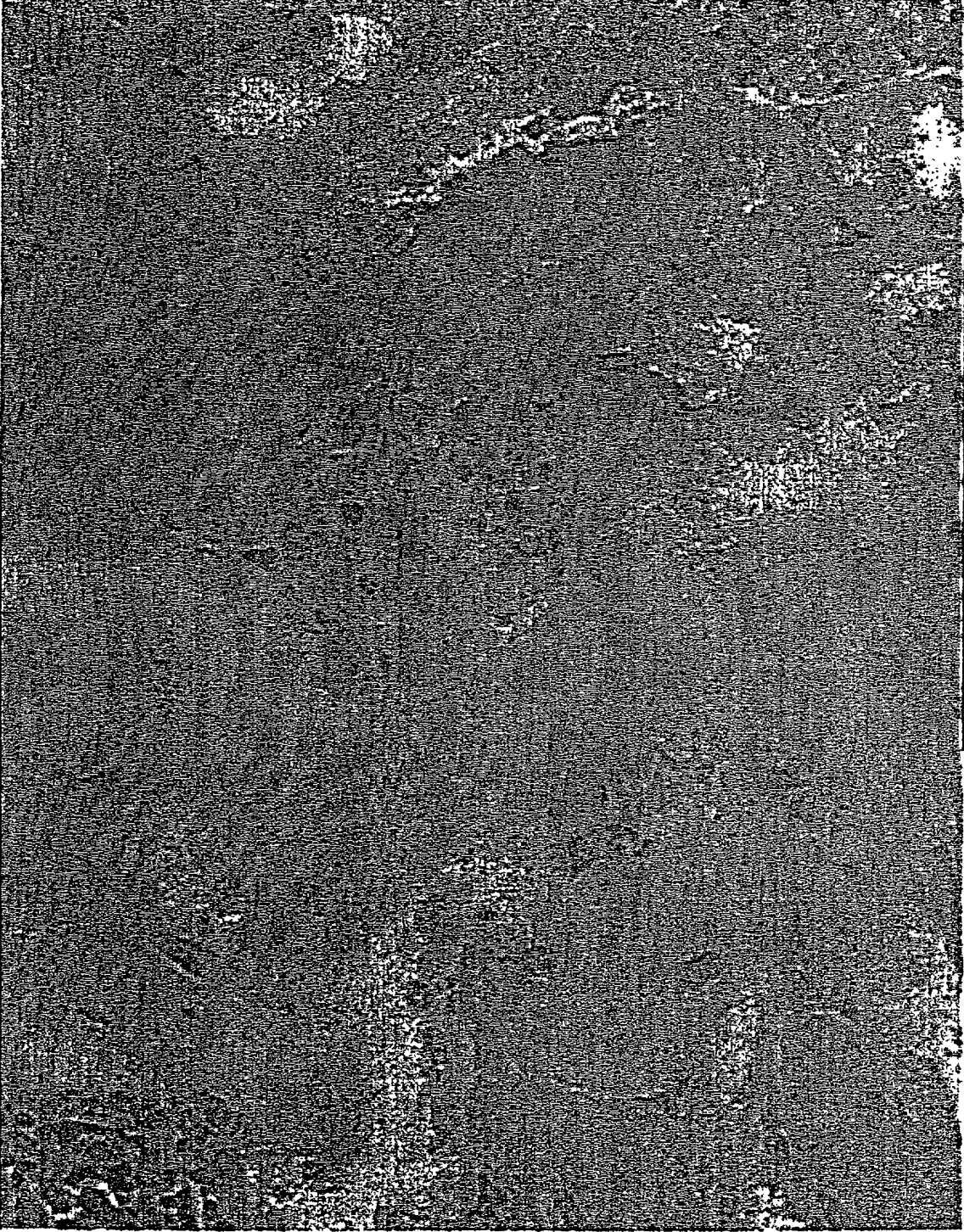


Fig. 3b

Fig. 3c



Mouse kidney, sagittal section

Fig. 3d

Mouse kidney, horizontal section



00413 04194



Mouse brain, sagittal section



Fig. 3e

**Mouse brain, coronary section**



**Fig. 3f**

Mouse brain, horizontal section

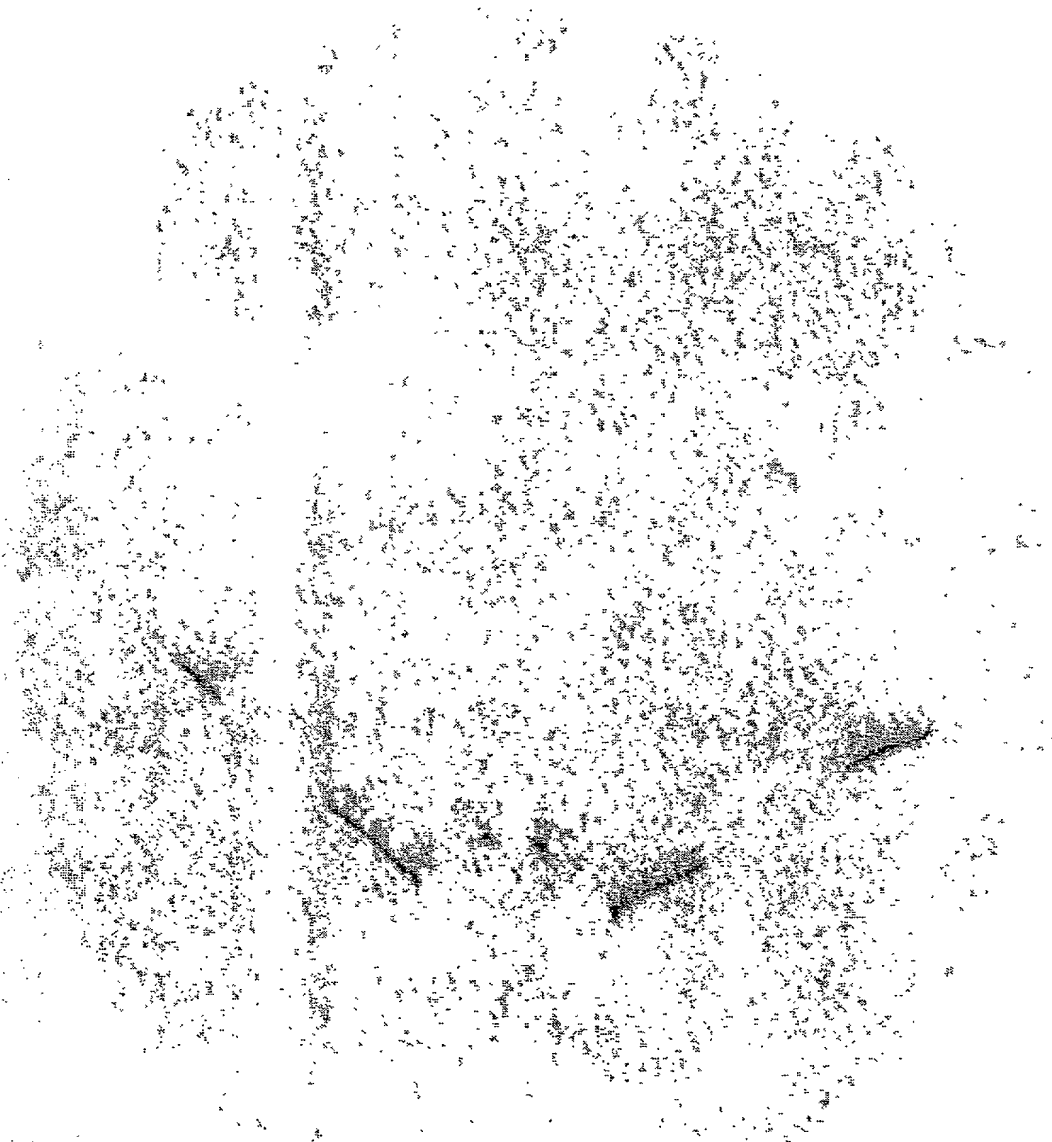


Fig. 3g

Mouse, choroid plexus

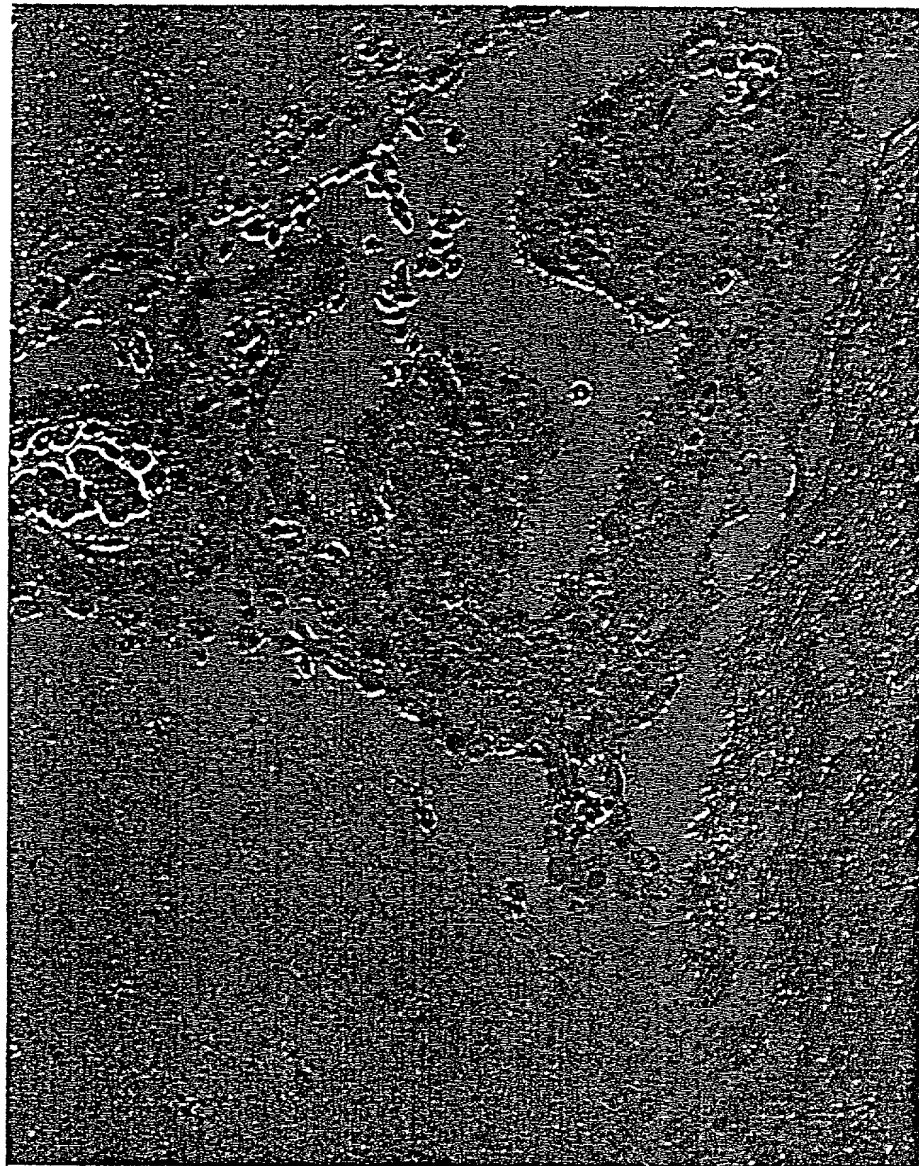


Fig. 3b



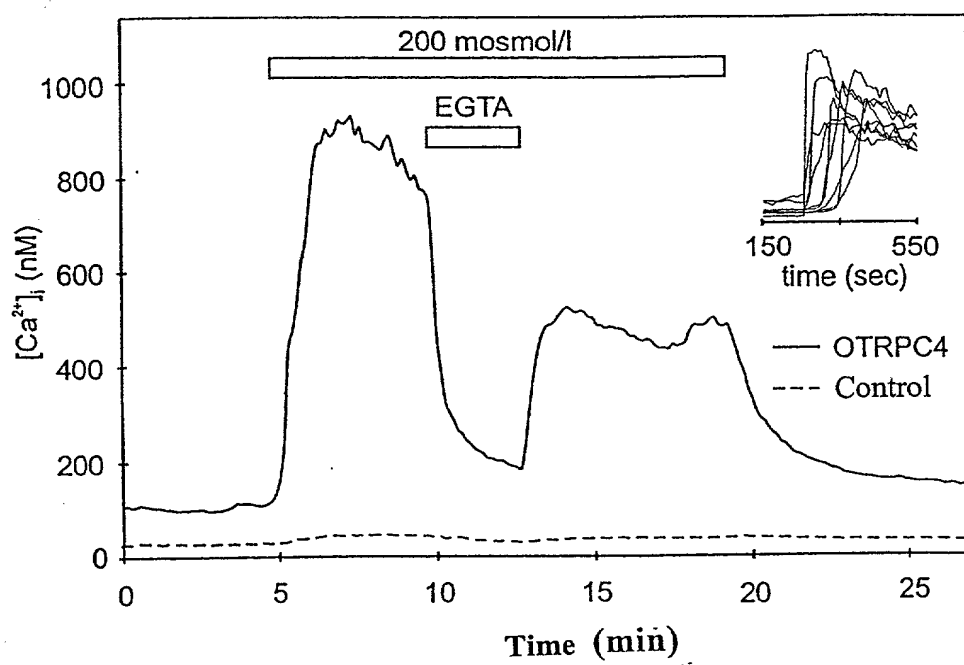


Fig. 4

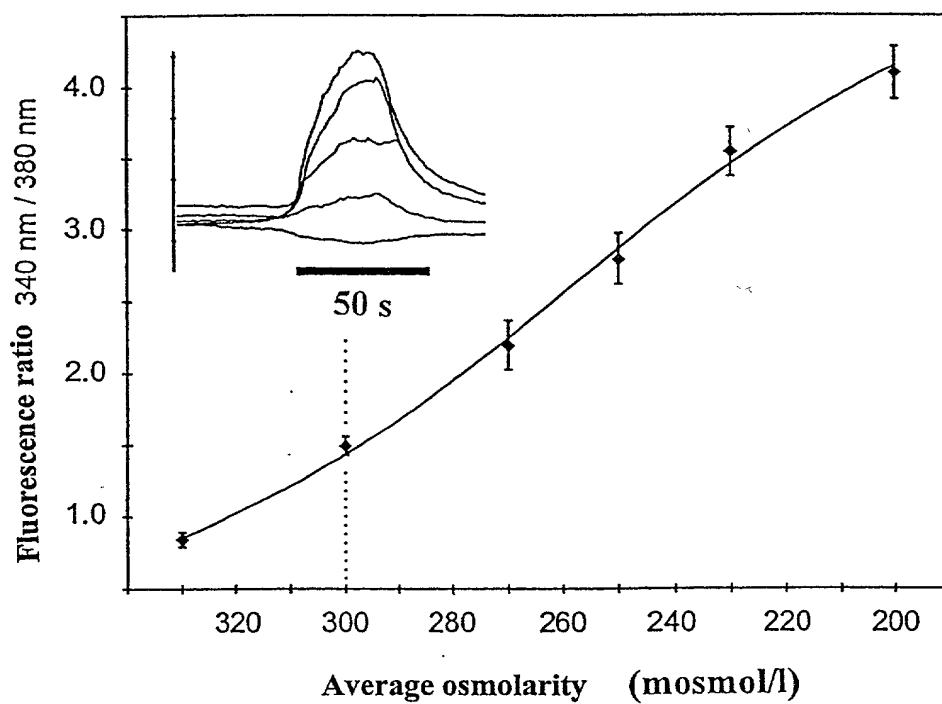


Fig. 5

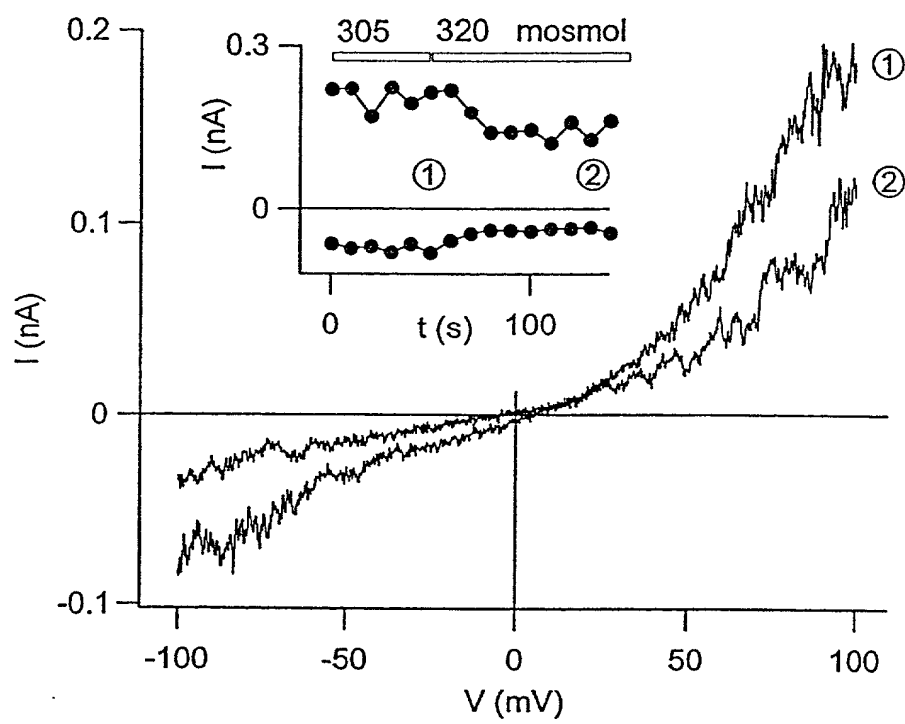


Fig. 6

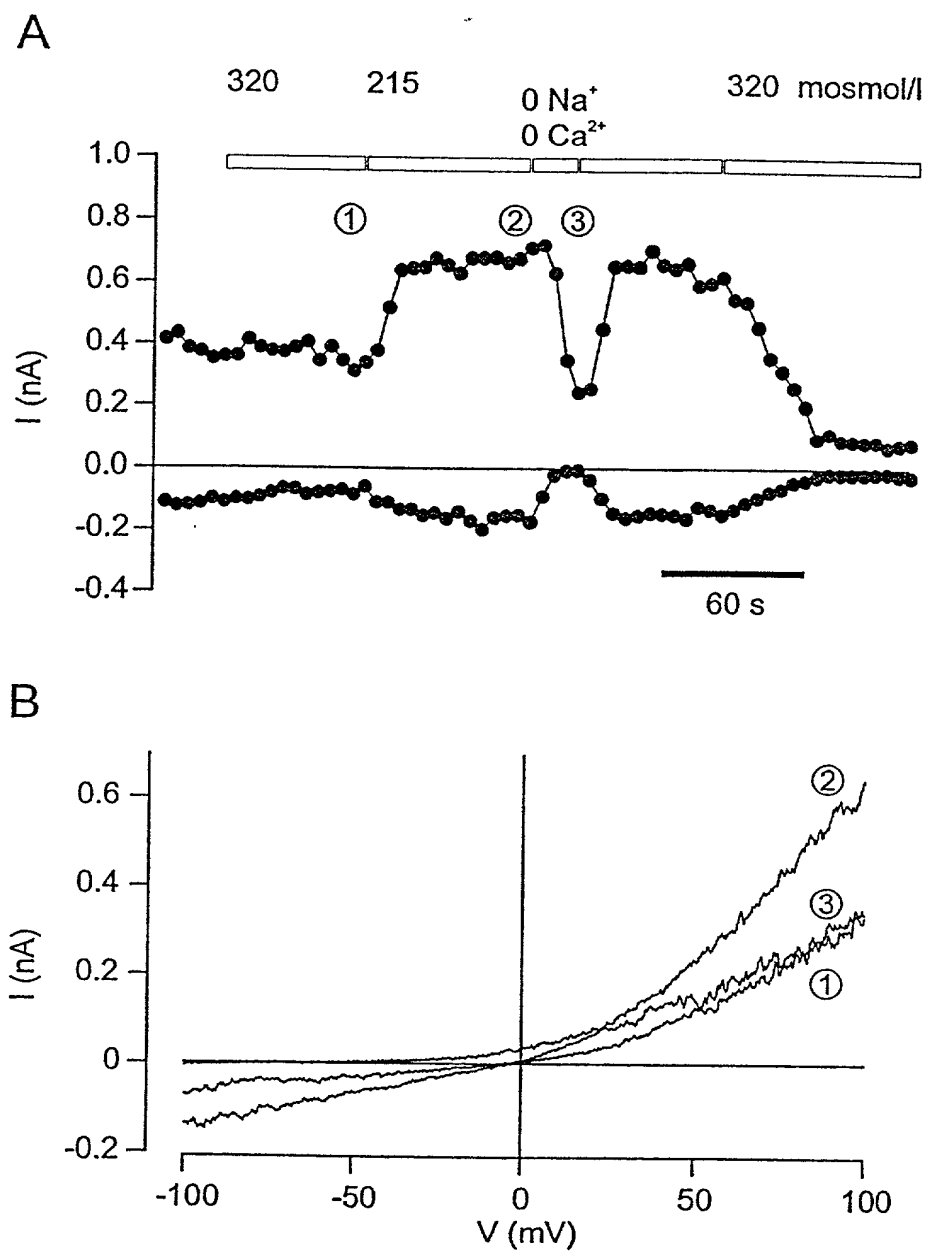


Fig. 7

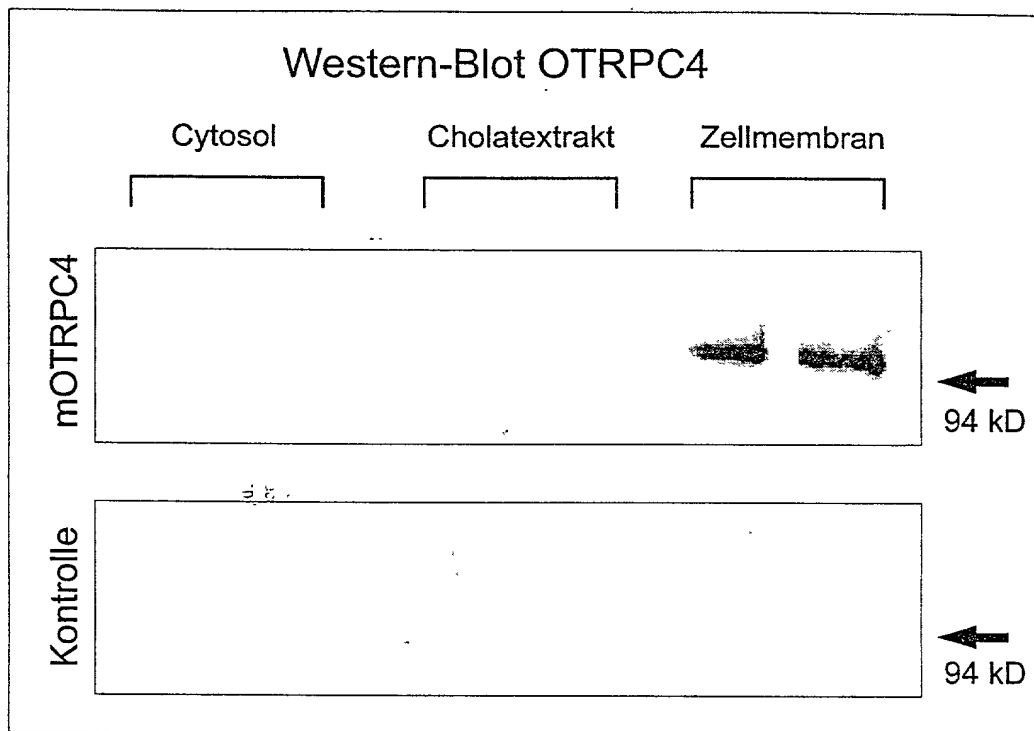


Fig. 2

# Calcium-abhängige Fluoreszenzänderungen an Fura-2 beladenen Plexus choroideus-Zellen

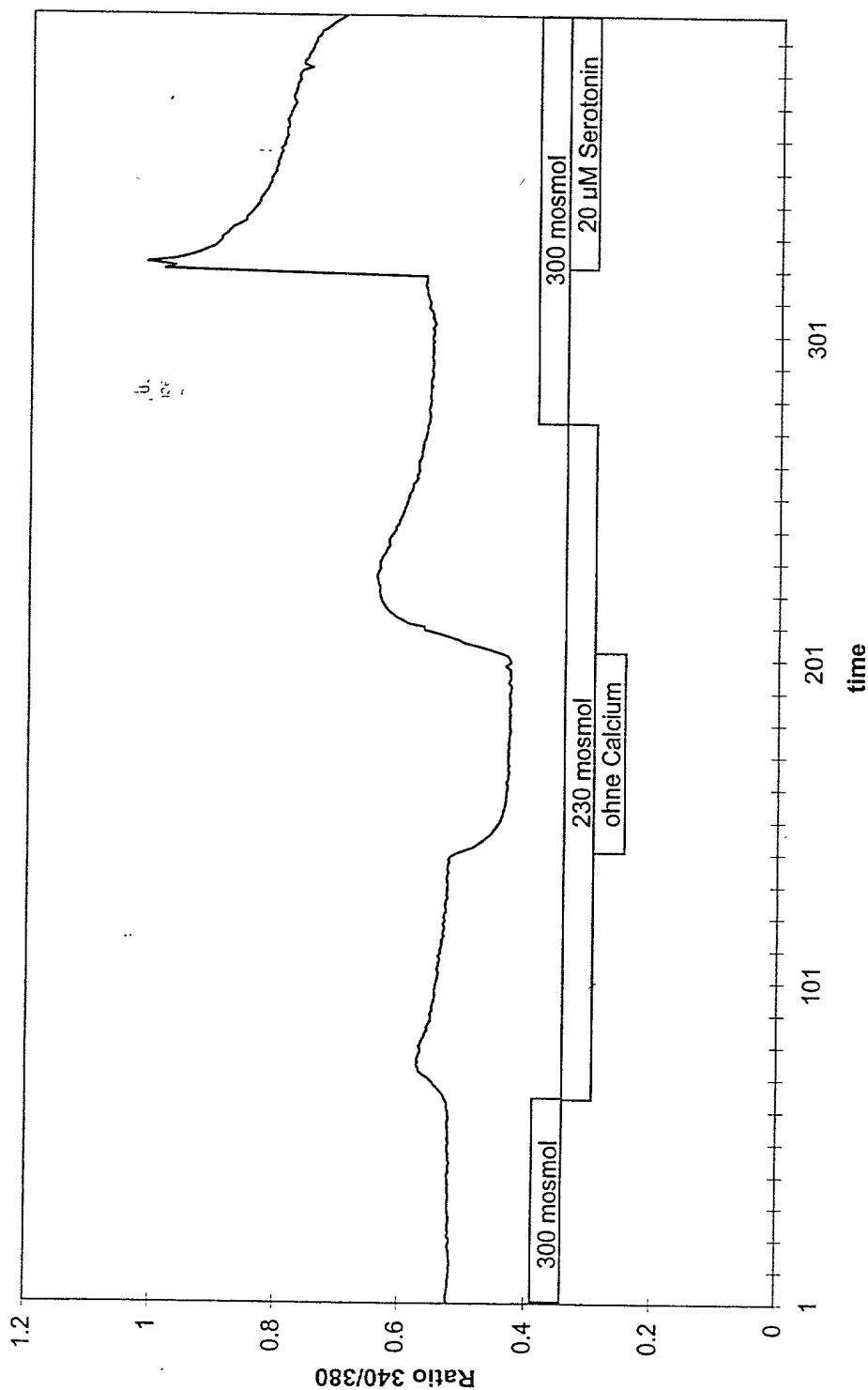
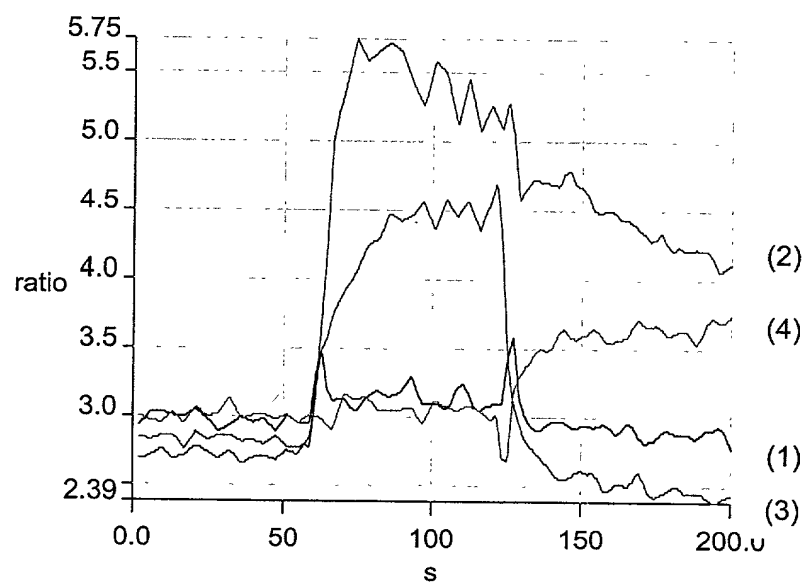


FIG. 9



- (1) Control
- (2) Ionomycin (2  $\mu$ M) EGTA
- (3) hypotonic solution (220 mosmol/l) EGTA
- (4) LOE908(100  $\mu$ M) hypotonic solution (220 mosmol/l)

Figure 10